

Figure 1A

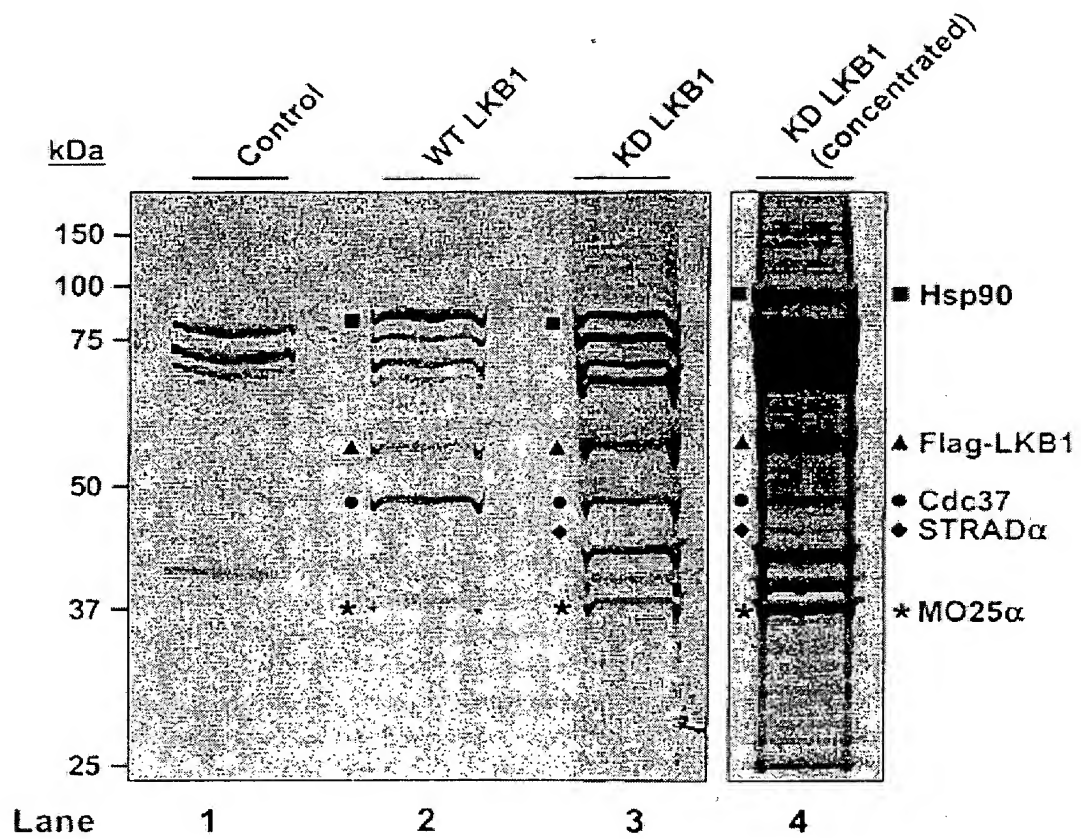


Figure 1B

	Protein name	Peptide matches	% sequence coverage	NCBI gi number
■	Hsp90	15/44	30%	20149594
▲	Flag-LKB1	14/46	35%	7106425
●	Cdc37	31/72	59%	5901922
◆	STRAD α	11/80	34%	12060855
*	MO25 α	17/37	47%	7706481

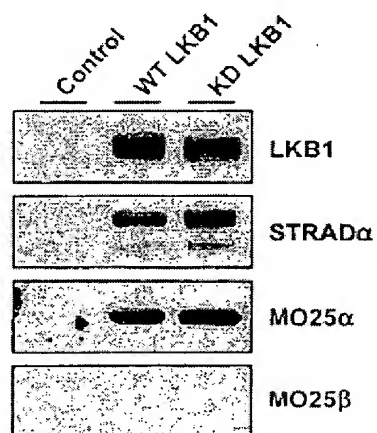
Figure 1C

Figure 2A

(SEQ ID NO:11) hMO25α	1	MPF-PFGKSHKSPADYVKNLKESIAILEKQD-----ISDKKAEKATEEVSKNLVA
(SEQ ID NO:12) hMO25β	1	MPL--FSKSHKNPAEIVKTLKENLAILEKQ-----DKKTEKASEEVSKSLQA
(SEQ ID NO:15) dMO25	1	MPL--FGKSKSEVSEVKSLEKALVALEAG-----DKKVEKACEEVSKNLVS
(SEQ ID NO:13) cMO25α	1	MLKPLFGKIDKPPADYVKNLKYALLVALEAG-----TNTSEKVEKALIEETKMLAL
(SEQ ID NO:14) cMO25β	1	MEL-LFGKSHKSPADYVKTLEVLTLLEKLPKPPKLDKDGNIQSDKKYKALIEVSKNLVA
(SEQ ID NO:11) hMO25α	50	MKEMLYGR--NEKEP-QTEAVAQLAQELYNSGLPSTLADLQILDFEGKKDVQAQIFNNIL
(SEQ ID NO:12) hMO25β	46	MKEMLCGH--NEKEP-PTAQAQLAQELYSSLLVTLADLQILDFEGKKDVQAQIFNNIL
(SEQ ID NO:15) dMO25	46	MKNMLYGS--SEAEPADYVVAQLAQELYNSNLLILILIONLHIDFEGKKHVAQIFNNIL
(SEQ ID NO:13) cMO25α	53	AKTFYVGEDANEPNN---EOMTQLAQEVVAVMLPFLIKHLHFPFECKKDVASEFNNIL
(SEQ ID NO:14) cMO25β	60	IKSFYVGNDSAEPSSEHVQVAQLAQELYNSNLLPFLIKMLPFPFECKKDVQAQIFNNIL
(SEQ ID NO:11) hMO25α	107	RRQIGTRSPVVEYICTOONILEMMLKGYE--SPETALNCGMLRECIHPLAKIILASE
(SEQ ID NO:12) hMO25β	103	RRQIGTRSPVVEYISAPHILEMMLKGYE--APQIALRCGMLRECIHPLAKIILASN
(SEQ ID NO:15) dMO25	104	RRQIGTRSPVVEYICTPEILFLMAGYEDAPPIALNSGMLRECIHPLAKIILHSE
(SEQ ID NO:13) cMO25α	110	RRQIGTRSPVVEYIAAPPEILLITLLKGYE--OPETALTCGMLRECIHPLAKIILASE
(SEQ ID NO:14) cMO25β	120	RRQIGTRSPVVEYIGARPEILLITLLKGYE--VETIALTCGMLRECIHPLAKIILASE
(SEQ ID NO:11) hMO25α	165	QRFDFFEVVEVSTFDIASDAFSTFKDLLTRHKILCAEFLEQHYDFF--SEVENILLSEN
(SEQ ID NO:12) hMO25β	161	QRFDFFEVVEVSTFDIASDAFSTFKDLLTRHKILVAFLEQHYDFF--EDYENILLSEN
(SEQ ID NO:15) dMO25	164	EFKFFFEVVEVSTFDIASDAFSTFKDLLTRHKILCAEFLDANYDFF--SQHYQILLSEN
(SEQ ID NO:13) cMO25α	168	YFQFFFEVVEVDVFDIASDAFSTFKDLLTRHKILCAEFLEQHYDFF--GOVSALTNSEN
(SEQ ID NO:14) cMO25β	178	VETFFELVVEVSEVFDIESDAFSTFKDLLTRHKILCAEFLEQHYDFF--AQVONILLSEN
(SEQ ID NO:11) hMO25α	224	VTRRQSLKLLGELLDRHNFNTMTKYISKPENLKLMMNLLRDKSRNIOFEAFHVFQVFA
(SEQ ID NO:12) hMO25β	220	VTRRQSLKLLGELLDRHNFNTMTKYISKPENLKLMMNLLRDKSRNIOFEAFHVFQVFA
(SEQ ID NO:15) dMO25	224	VTRRQSLKLLGELLDRHNFNTMTKYISEPENLKLMMNLLRDKSRNIOFEAFHVFQVFA
(SEQ ID NO:13) cMO25α	227	VTRRQSLKLLGELLDRHNFNTMTKYIISPENLKLMMNLLRDKSRNIOFEAFHVFQVFA
(SEQ ID NO:14) cMO25β	237	VTRRQSLKLLGELLDRHNFNTMTKYISNPENLKLMMNLLRDKSRNIOFEAFHVFQVFA
(SEQ ID NO:11) hMO25α	284	NPNKTOPIEDILLRNCALKEFLSKGFNDRTDEQFNDEKAYLIKQIELKRPAAQEA--
(SEQ ID NO:12) hMO25β	280	SPHKTOPIEDILLRNCALKEFLSKGFNDRTDEQFNDEKAYLIKQIELKRPAAQEA--
(SEQ ID NO:15) dMO25	284	NPNKPEPIEDILLRNCALKEFLSKGFNDRTDEQFNDEKAYLIKQIELKRPAAQEA--
(SEQ ID NO:13) cMO25α	287	NPNKPEPIEDILLRNCALKEFLSKGFNDRTDEQFNDEKAYLIKQIELKRPAAQEA--
(SEQ ID NO:14) cMO25β	297	NPNKPEPIEDILLRNCALKEFLSKGFNDRTDEQFNDEKAYLIKQIELKRPAAQEA--
(SEQ ID NO:11) hMO25α		-----
(SEQ ID NO:12) hMO25β		-----
(SEQ ID NO:15) dMO25		-----
(SEQ ID NO:13) cMO25α		-----
(SEQ ID NO:14) cMO25β	357	KSKEDENQEPAGPSEGPSTSQ

Figure 2B

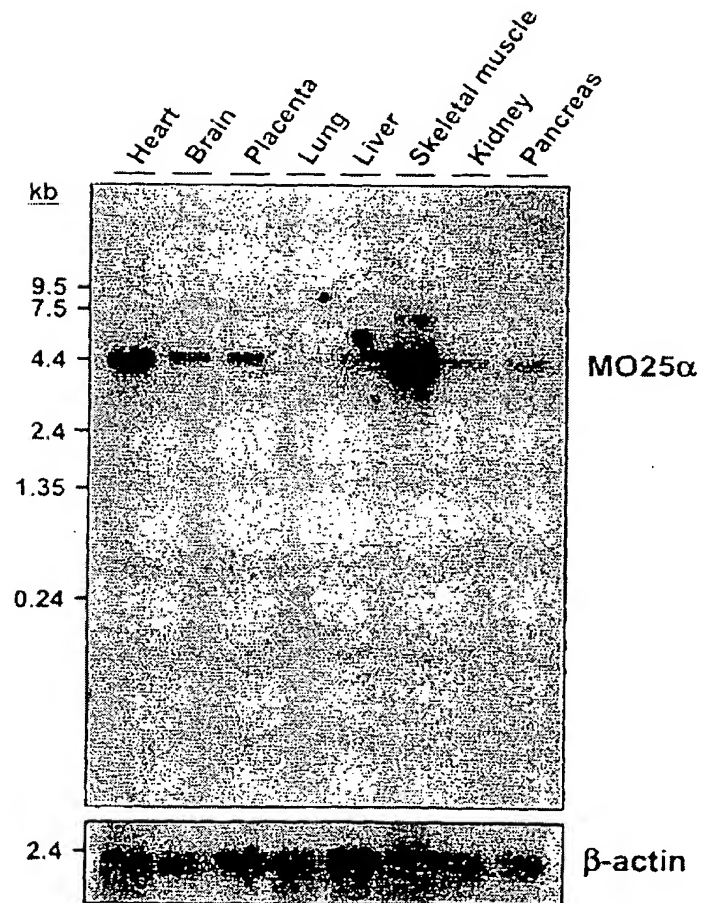


Figure 2C

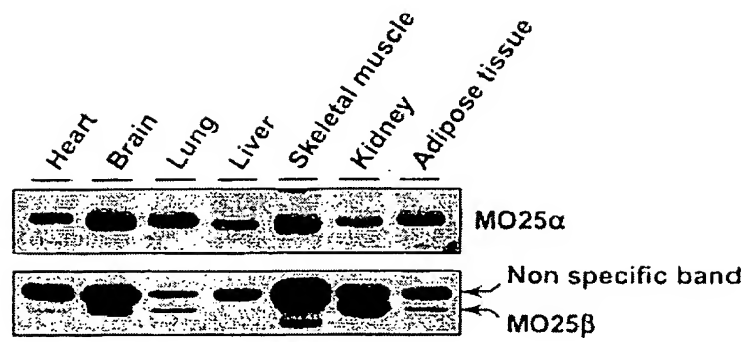


Figure 2D

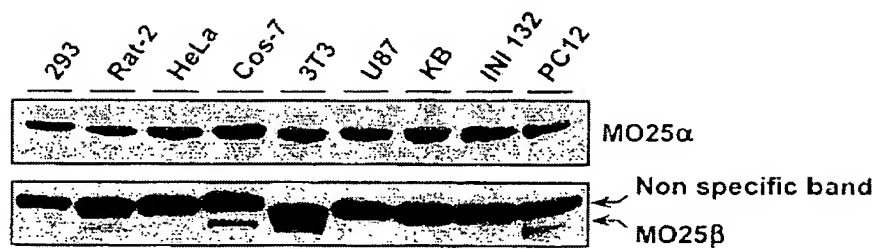


Figure 4A

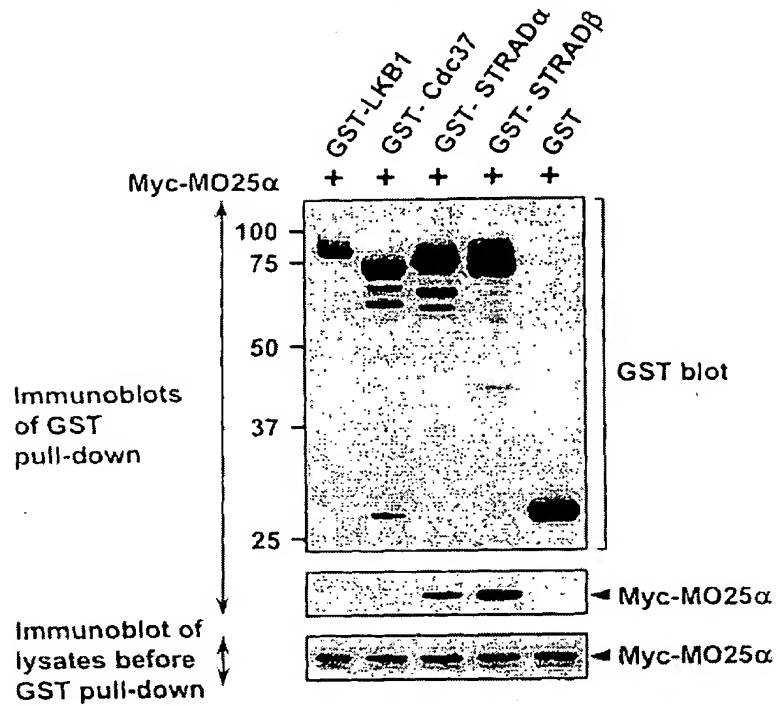


Figure 4B

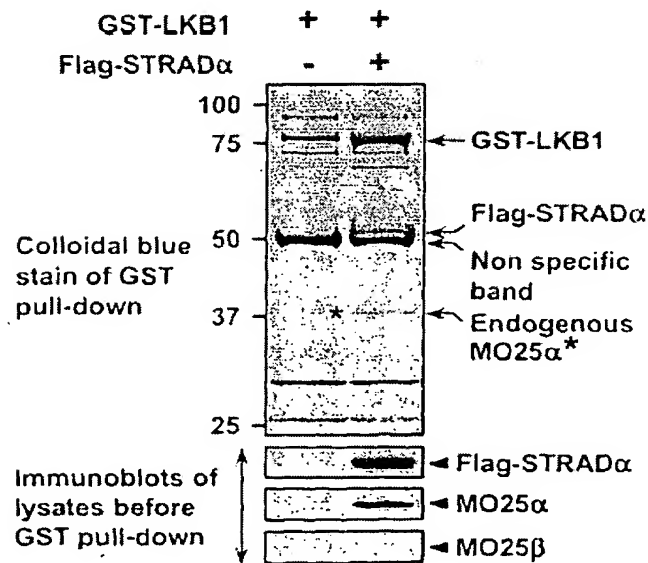


Figure 4C

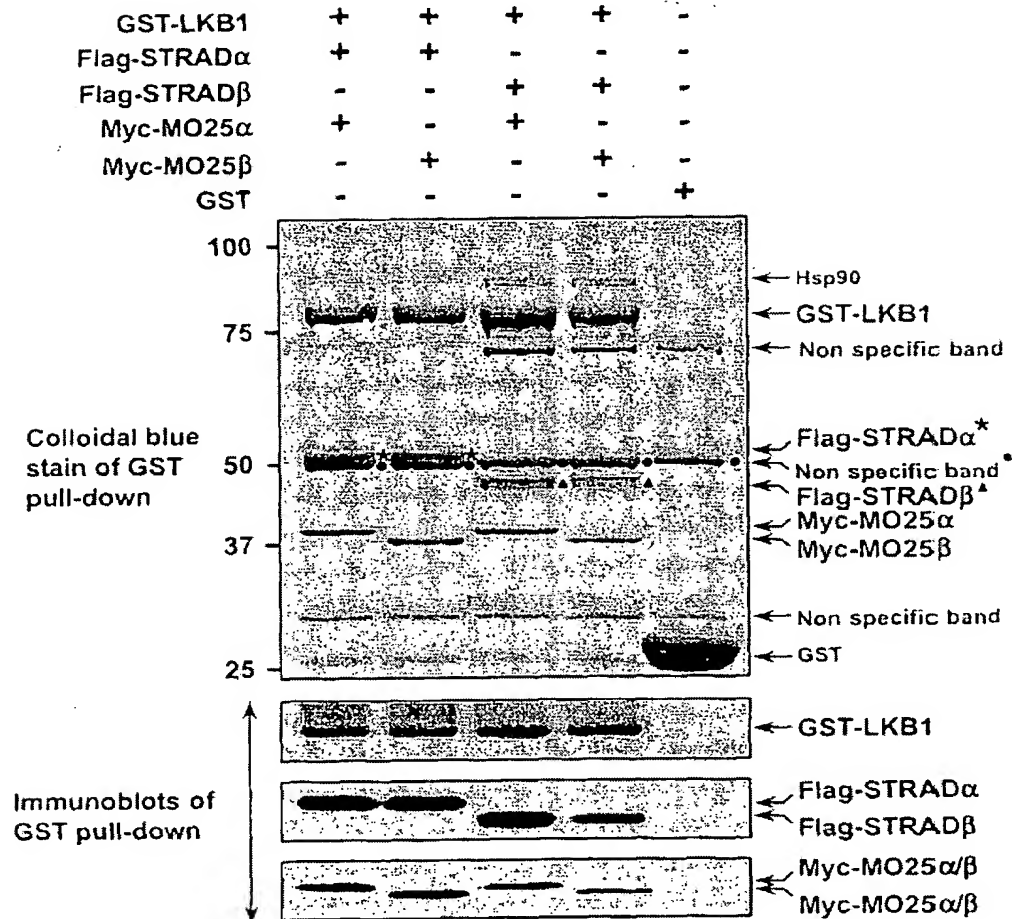


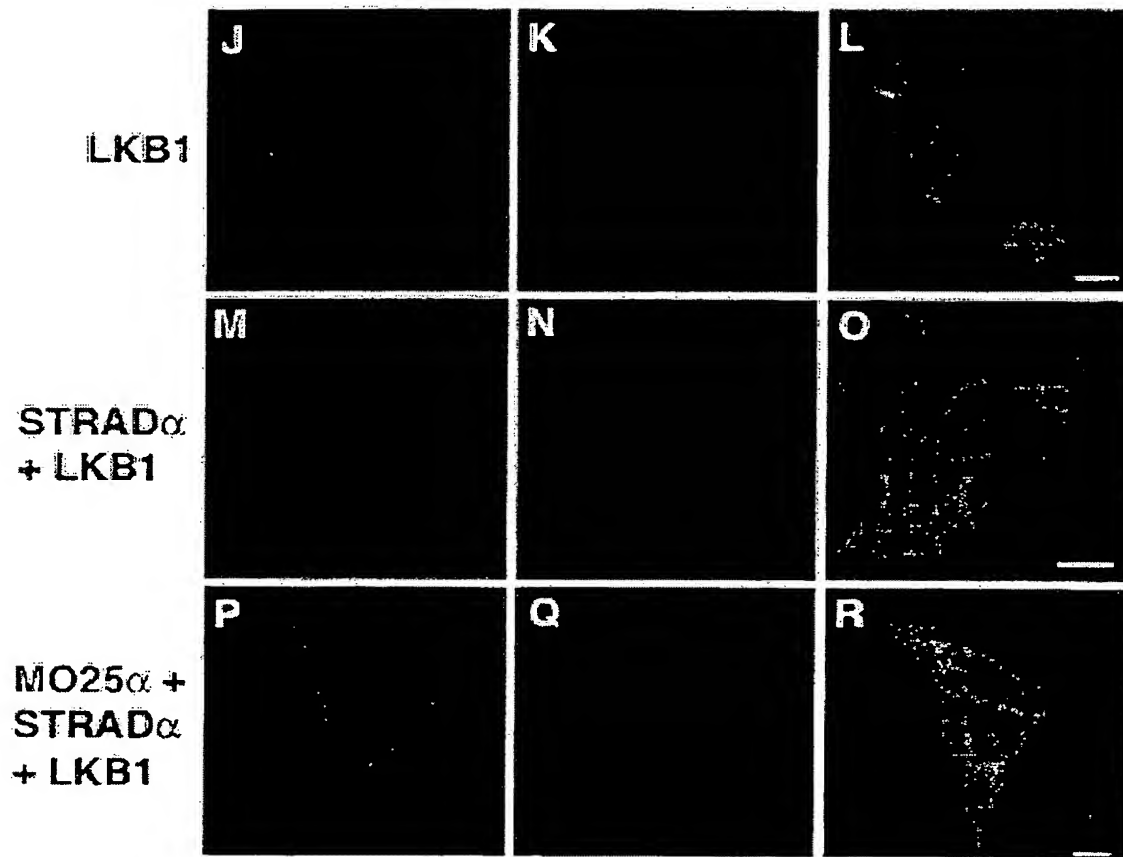
Figure 5 (continued)

Figure 6A

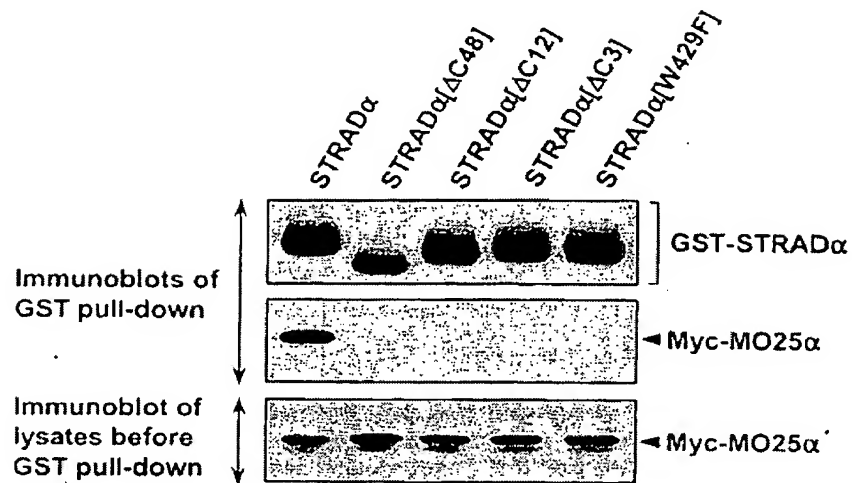


Figure 6B

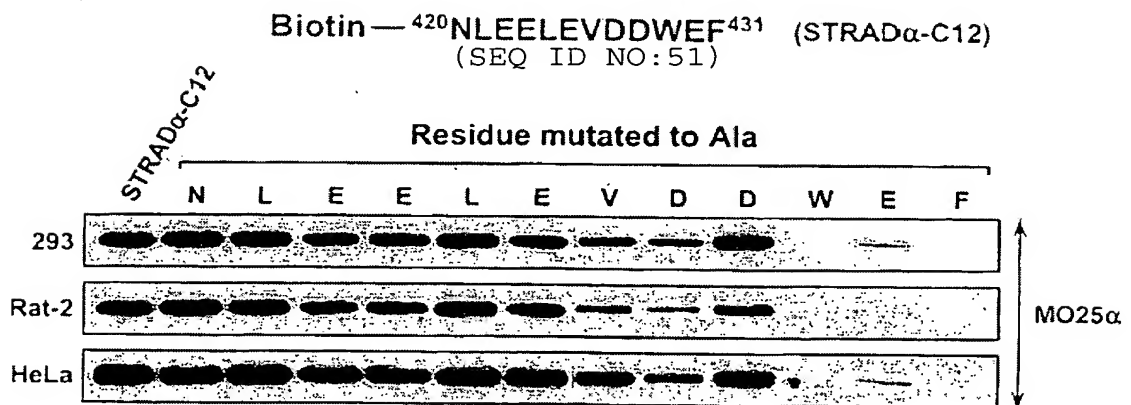


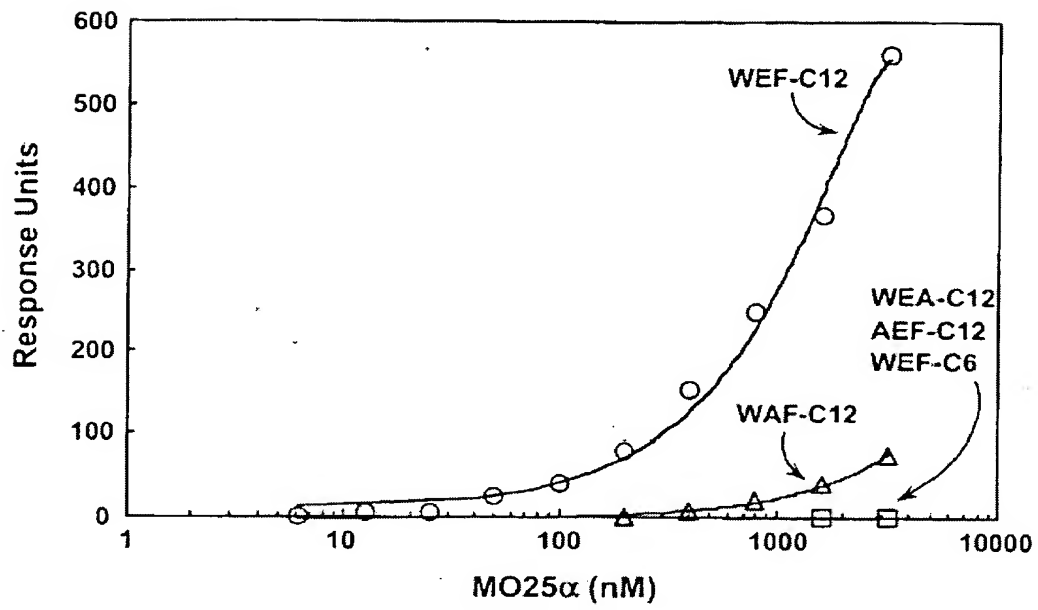
Figure 6C

Figure 10

(SEQ ID NO:9) hSTRAD α 1 MSFLVSKPERIRRVSEKFIVEGLRDLFLFGEQPPGDTIRKNTDASSESIASFSKQEVMS
(SEQ ID NO:10) hSTRAD β 1 -----MSLDDQCSSTOVESLRPEK-----QSETSILOYLVDEPTLSWSRSPSTRASEV
(SEQ ID NO:56) hSPAK 1 -----MAEPSPGVHVLQPCQAAPPTAAAAAPAAATAAPAPAPAPAPAPAPAPAPAPAAQAV
(SEQ ID NO:57) hOSR1 1 -----MSEDSSAE

(SEQ ID NO:9) hSTRAD α 61 SLLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTRINLEACSNENVTFLQGEH
(SEQ ID NO:10) hSTRAD β 50 LCSTNVSHYELQVEIGRGFFNLTSVHLARHTPTGTLVTIKITNLENCNEERLKALQKAVI
(SEQ ID NO:56) hSPAK 57 GNPICRDAYELQVEIGSG--ATAVVOAALCKPCRERVAIKRINLEKCQTSMDDELLK-EIQ
(SEQ ID NO:57) hOSR1 9 PWSINRDDYELQVEIGSG--ATAVVOAAYCAPKKEVVAIKRINLEKCQTSMDDELLK-EIQ

(SEQ ID NO:9) hSTRAD α 121 VSKLFNHPNIVPYRAIFLADNELWVTSFPAAYGSARDLICTHFMDC-----INELATAY
(SEQ ID NO:10) hSTRAD β 110 LSHFFNHPNITTVETVFTVGSWLVNISPFPAYGSASQERTTYFPEG-----MSEIRN
(SEQ ID NO:56) hSPAK 114 AMSQCSPNIVTYTTSFVVKDELWVMKLLSGGSMLEIKYIVNRGEHKNGVDEEATAT
(SEQ ID NO:57) hOSR1 66 AMSQCSPNIVSYTTSFVVKDELWVMKLLSGGSLDIKHIIVAKGEHKSVMDEETAT

(SEQ ID NO:9) hSTRAD α 175 ILQCVLKALDYTHFMGYVHRSVKASHILLSVDGKVVYSGLRNSLSLISHGORQRVVHDFP
(SEQ ID NO:10) hSTRAD β 164 ILFGANRGLNYLHONGCIHRSFKASHILLSGDLVTSLSLHLSLVKHGORHRAVYDFP
(SEQ ID NO:56) hSPAK 174 ILREVLEGLDYLHNGQIHRRDKKGNILLGEDGSVOLADFGVSAFLATCGDVTR--NKVR
(SEQ ID NO:57) hOSR1 126 ILREVLEGLDYLHNGQIHRRDKKGNILLGEDGSVOLADFGVSAFLATCGDITR--NKVR

(SEQ ID NO:9) hSTRAD α 235 KYSVKVLPWTSPEVEGONEQGYDAKSDIYVSGITACELANGHVPEKOMPATOMLEKLNK
(SEQ ID NO:10) hSTRAD β 224 QFSTSVQPVLSPEVRODLYGYNVKSDIYVSGITACELASGOVPEQDMHRTQILLQKLKG
(SEQ ID NO:56) hSPAK 232 KTFVGTFCWMAPEVNEC--VRGYDFKADMSFGITATELATGAAPPHKYPPMKVLLTLN
(SEQ ID NO:57) hOSR1 184 KTFVGTFCWMAPEVNEC--VRGYDFKADMSFGITATELATGAAPPHKYPPMKVLLTLN

(SEQ ID NO:9) hSTRAD α 295 ---TTP-----CLL-DTSTIPAEELTSPSRSVANSGL-SDSL
(SEQ ID NO:10) hSTRAD β 284 -PPYSP-----L--DISIFPQESRKNSSQSGVDSGIGESVL
(SEQ ID NO:56) hSPAK 291 DPPTLETGVQDKEMKKYKGSFRKMSLCLQKDPKRPETADELKCKKPKAKNR-EVLT
(SEQ ID NO:57) hOSR1 243 DPPSLETGVQDKEMKKYKGSFRKMSLCLQKDPKRPETADELKHQPKAKNK-ETLQ

(SEQ ID NO:9) hSTRAD α 328 TTSTPRPSNGDWPSPYHRT--FSPPHHIFVEQCLORNPDARPSASTLLNHSEFKQIKRR
(SEQ ID NO:10) hSTRAD β 318 VSSGTHIVNSDRLHTPSSKT--FSPAFFSLVQLCLOQDPEKRPASASSLLSHVFFKOMKEE
(SEQ ID NO:56) hSPAK 350 EKLLTRTPPIAQRKKVRRVPGSSCHLHKTEDGGWENSDDDEKSEEGKAARSQEKSR
(SEQ ID NO:57) hOSR1 302 EKLLQRPPTISPRAKKVVRRVPGSSCHLHKTEDGGWENSDDDEKSEEGKAARSQELRSPR

(SEQ ID NO:9) hSTRAD α 386 ASK-----AIPELERP-----VTPITME
(SEQ ID NO:10) hSTRAD β 376 SQD-----SILSLIP-----PAY
(SEQ ID NO:56) hSPAK 410 VKE--ENPETAVSAS-----IPECHQS-----PSVHDSQGFPPNANEDV
(SEQ ID NO:57) hOSR1 362 VKESISNSEEFPITDPVGTLLQVPEQISAHLPQAPAGQIATOPTQVSEPPPAEPKTAQAL

(SEQ ID NO:9) hSTRAD α 404 EGSQ-S---QDHSCHFGFLVTNLEELEVDDEEF-----
(SEQ ID NO:10) hSTRAD β 389 NKFSIS---LPPVLWPTEPECDFPEKDSYMEF-----
(SEQ ID NO:56) hSPAK 447 REAS-S---CAVNLVLRRLNSKELNDIRFEFTPGRDTAGVQSQELFSAGLVDGHDVVI
(SEQ ID NO:57) hOSR1 422 SSGSGSQETKIPISLVLRLRNSKELNDIRFEFTPGRDTAGVQSQELFSAGLVDGHDVVI

(SEQ ID NO:9) hSTRAD α -----
(SEQ ID NO:10) hSTRAD β -----
(SEQ ID NO:56) hSPAK 502 VAANLQKIVDEPKALSTTFKLASGCGSEIPDEVKLIGFAQLSFS
(SEQ ID NO:57) hOSR1 482 VAANLQKIVDEPKALSTTFKLASGCGSEIPDECKLIGFAQLSFS

Figure 12

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(SEQ ID NO:58) Tos3      11  ..LPRSSLLYNNASNSSSRIKETRKVKLLYNELTKR.....Q...ILNNFEILATLGNQG
(SEQ ID NO:59) Pak1      94  ..TPTTTSSFCSSGSSKNKVEETNRISLTYDPVSKR.....K...VLNTYEIIKELGHGQ
(SEQ ID NO:61) CaMKKβ    121 CICPSLPYSPVSSPQSSPRLPRRPTVESHVHSITGM.....QDCVQLNQYTLKDEIGKGS
(SEQ ID NO:6)  LKB1       7   QQLGMFTGELMSVGMDFIHRIDSTEVIYOP..RR.....KRAKLIGKYLMDLLGEGS
(SEQ ID NO:60) Elm1      39  TSSFGSSFSQQKPTYSTIIGENIHTILDEIRPYVKKITVSDQDKKTINQYTLGVSAGSQQ
(SEQ ID NO:62) consensus 121  p s s s s s rik tv l y pltkr q ilnny i lg Gq

(SEQ ID NO:58) Tos3      61  YGKVKLARDLGTGALVAIKILNRFEKRS....GYSL.....QLKV.EN.....
(SEQ ID NO:59) Pak1     144  HGKVKLARDILSKQLVAIKIVDRHEKKQRKFFTFIK.....SSKISEN.....
(SEQ ID NO:61) CaMKKβ    176 YGVVKLAYNENDNTYYAMKVLK..KKLIRQAGFPR.....RPPPRGTRPAPGGCIQF
(SEQ ID NO:6)  LKB1      60  YGKVKELVDSETLCRRRAVKILK..KKLRR.....
(SEQ ID NO:60) Elm1     99  FGYVRKAYSSTLGKVVAVKIIIPKPEWNAQQYQSVNQVMRQIQWLWKSQKITTMSGNEAMR
(SEQ ID NO:62) consensus 181 yGkVkla d t lvAiKi l k k k y k

(SEQ ID NO:58) Tos3      99  ....PRVNOEIEVMKRCHHE.NVVELYEILNDPESTKVYLVLEYCSRGPVKWCPCENKMEI
(SEQ ID NO:59) Pak1     187  ....DKIKREIAIMKKCHHK.HVVQLIEVLDDLSRKIYLVLEYCSRGEVVKWCPDCMES
(SEQ ID NO:61) CaMKKβ    227 RGPTEQVYQEIAILKKLDHP.NVVKLVEVLDDPNEDHLYMVFEVLVNGQPV.....MEV
(SEQ ID NO:6)  LKB1      89  PNGEANVKKEIQLLRLRHK.NVIQLVDVLYNEEKQKMYMVMEYC.....VCGMQEM.L
(SEQ ID NO:60) Elm1     159 LMNIEKCRWEIFAASRLRNVHIVRLIECLDSPFSESIWIVTNWCSLGELQWKRDDDEDI
(SEQ ID NO:62) consensus 241 drvk EI vmkrlhh nvv LlievLddp s kvylVleycs g v wc mei

(SEQ ID NO:58) Tos3     154  .KAVGPSILTFQQ...SRKVVLDDVSGLEYLHLSQGITHRDIKPSNLLISSNGTV.KISD
(SEQ ID NO:59) Pak1     242  .DAKGPSLLSFQE....TREILRGVVLGLEYLHYOGI IHRDIKPANLLISGDGTV.KISD
(SEQ ID NO:61) CaMKKβ    279 .PTLKE..LSEDQ....ARFYFQDLIKGIEYLHYQKIIHRDIKPSNLLVGEDGHI.KIAD
(SEQ ID NO:6)  LKB1     141  .DSVPEKRFPVCQ....ANGYFCQLIDGLEYLHLSQGIHVHKDIKPGNLLLTGGTTL.KISD
(SEQ ID NO:60) Elm1     219 LPQWKKIVISNCSVSTFAKKILEDMTKGLEYLHLSQGCIIHRDIKPSNILLDEEEKVAKLSD
(SEQ ID NO:62) consensus 301 v p ils q ar vv dvv GLEYLHsQgiiHrDIKPSnllis dgtv KisD

(SEQ ID NO:58) Tos3     208 FG..VAM.STATGSTNIQSSHEQLLKSRA LGTPAFFAPELCSTEKEY.....
(SEQ ID NO:59) Pak1     296 FG..VSLAASSTNSSDSSESLELELAKTVGTPAFFAPEMCLGEDAFTRYNLTKENLFRG
(SEQ ID NO:61) CaMKKβ    331 FG..V.....SNEFKGS..DALLSNTVGTPAFMAPESLS.....ETRKIFSG
(SEQ ID NO:6)  LKB1     195 LG..VAEALHPFAADDTCTRSQ.....GSPAQFPPEIANGLDTFSS.....
(SEQ ID NO:60) Elm1     279 FGSCIFTPLQSLPFSDFANFEDCFQRELNKIVGTPAFIAPELCHLGNKSRDFVTD.....
(SEQ ID NO:62) consensus 361 fG v t s d s l r vGtPAF aPElc y

(SEQ ID NO:58) Tos3     252 SC.SSAIDIWSLGVTIYCLLFGKLPFNANSGLELFDISIINKPLEFSPSYEEMLNATSGIT
(SEQ ID NO:59) Pak1     354 SCISFMIDIWAVGVTLYCLLFGMLPFFSDFELKLFKEKIVNDPLKFPTFKEIQSNKVSQVS
(SEQ ID NO:61) CaMKKβ    369 K....ALDVWAMGVTLYCFVFGQCPFMDERIMCLHSHKIKSQALEFPDQPDIA.....
(SEQ ID NO:6)  LKB1     233 ...GFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGKGSYAIP.....
(SEQ ID NO:60) Elm1     332 ...GFKLDIWSLGVTIYCLLYNELPFFGENEFETYHKIIEVSLSSKINGNTLNDLVIKRL
(SEQ ID NO:62) consensus 421 f iDiWslGVTLlycllfg lPf ad l lfdkIi l fp em

(SEQ ID NO:58) Tos3     311 M.EEYT...DAKDLLKKLLQKDPDKRIKLADIKVHPFMC....HYGKSDAASVL...TN
(SEQ ID NO:59) Pak1     414 CEEYE...MAKDLLKKLEKNPQKRMTIPAIKKHFFVS.WDFDHVPENDEKLLS...SV
(SEQ ID NO:61) CaMKKβ    417 .....E...DLKDITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTE
(SEQ ID NO:6)  LKB1     276 .GDCGP...PLS DLLKGMLEYEPAKRFSIRQIROHSWFRK...KHPPAEAPVPIPPSPDT
(SEQ ID NO:60) Elm1     389 LEKDVTLRISIQDLVKVLSRDQPIDSRNHSQISSSS.VNPVRNEGVPVRRFFGRLLTKKKG
(SEQ ID NO:62) consensus 481 ee lkDLlkkllleknP kri l Ik hpfv dh p d vl t

(SEQ ID NO:58) Tos3     359 LETFHELKVSP.....SSCKRVELVSLPVNSSFASLDSVYMFNDHNNLRTGADRNS
(SEQ ID NO:59) Pak1     467 LE..QKLRF.....QCNQTDQFE.PISISKHELKNAV.....SGVGKKIKESV
(SEQ ID NO:61) CaMKKβ    469 EEVENSVKHIPSLATVILVKTMIKRSPGNPFEGSRREERSLSAPGNLLTKQGSEDNLQK
(SEQ ID NO:6)  LKB1     329 KDRWRSMTVVYPYLEDLHGADEDEDLFDIEDDIYTDQFTVPGQVPEEEASHNGQRRLPG
(SEQ ID NO:60) Elm1     448 KKTSGKGKDKVLVSATSKVTPSIHIDEEDPKECFSTTVLRSSPDSSDYCSSLGEAIOVT
(SEQ ID NO:62) consensus 541 e lk p l rve pv s lks s lg

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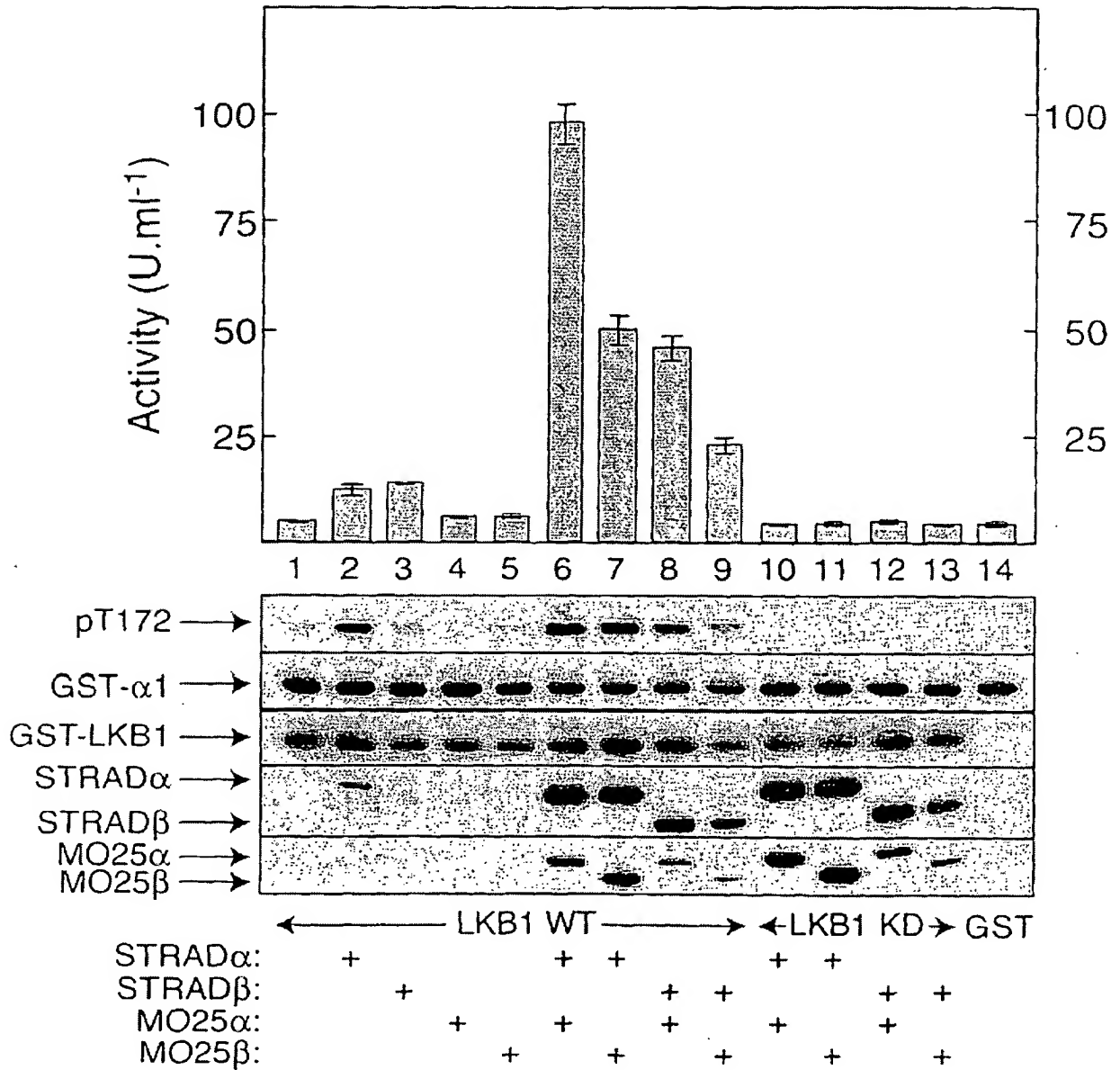
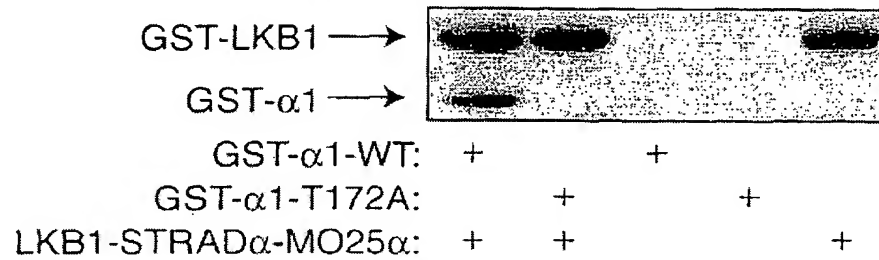
Figure 15AActivation of AMPK α 1 catalytic domain by LKB1

Figure 15B

Phosphorylation of AMPK α 1 catalytic domain by LKB1



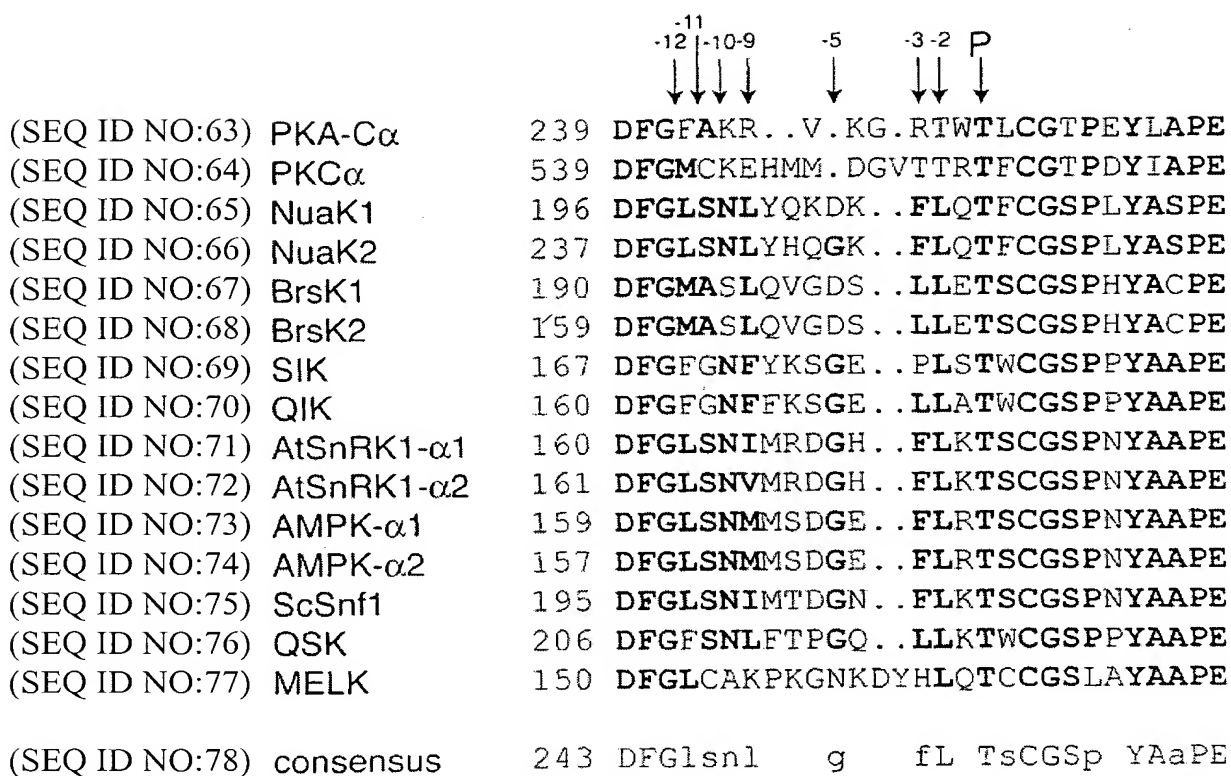
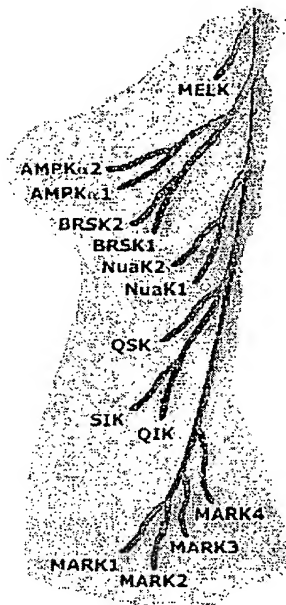


Figure 21A



(SEQ ID NO:73)	AMPK1	159-	DFGLSNMMSDGE--FLRTS	*	CGSPNYAAPE
(SEQ ID NO:74)	AMPK2	157-	DFGLSNMMSDGE--FLRTS	*	CGSPNYAAPE
(SEQ ID NO:67)	BRSK1	174-	DFGMASEQVGDS--LLETSC		CGSPHYACPE
(SEQ ID NO:68)	BRSK2	159-	DFGMASEQVGDS--LLETSC		CGSPHYACPE
(SEQ ID NO:65)	NUAK1	196-	DFGLSNLYQKDK--FLQTE		CGSPLYASPE
(SEQ ID NO:66)	NUAK2	193-	DFGLSNLYHQGK--FLQTE		CGSPLYASPE
(SEQ ID NO:69)	SIK	167-	DFGFGNFFKSGE--PLST		CGSPPYAAPE
(SEQ ID NO:70)	QIK	160-	DFGFGNFFKSGE--LLATW		CGSPPYAAPE
(SEQ ID NO:76)	QSK	206-	DFGFSNGLTIPGQ--LLKTW		CGSPPYAAPE
(SEQ ID NO:79)	MARK1	200-	DFGFSNEETVGN--KLDTE		CGSPPYAAPE
(SEQ ID NO:80)	MARK2	160-	DFGFSNEETVGN--KLDTE		CGSPPYAAPE
(SEQ ID NO:81)	MARK3	196-	DFGFSNEETVGG--KLDTE		CGSPPYAAPE
(SEQ ID NO:82)	MARK4	198-	DFGFSNEETLGS--KLDTE		CGSPPYAAPE
(SEQ ID NO:77)	MELK	150-	DFGLCAKPKGKNKDYHLQTC		CGSLAYAAPE

29/38

Figure 21B

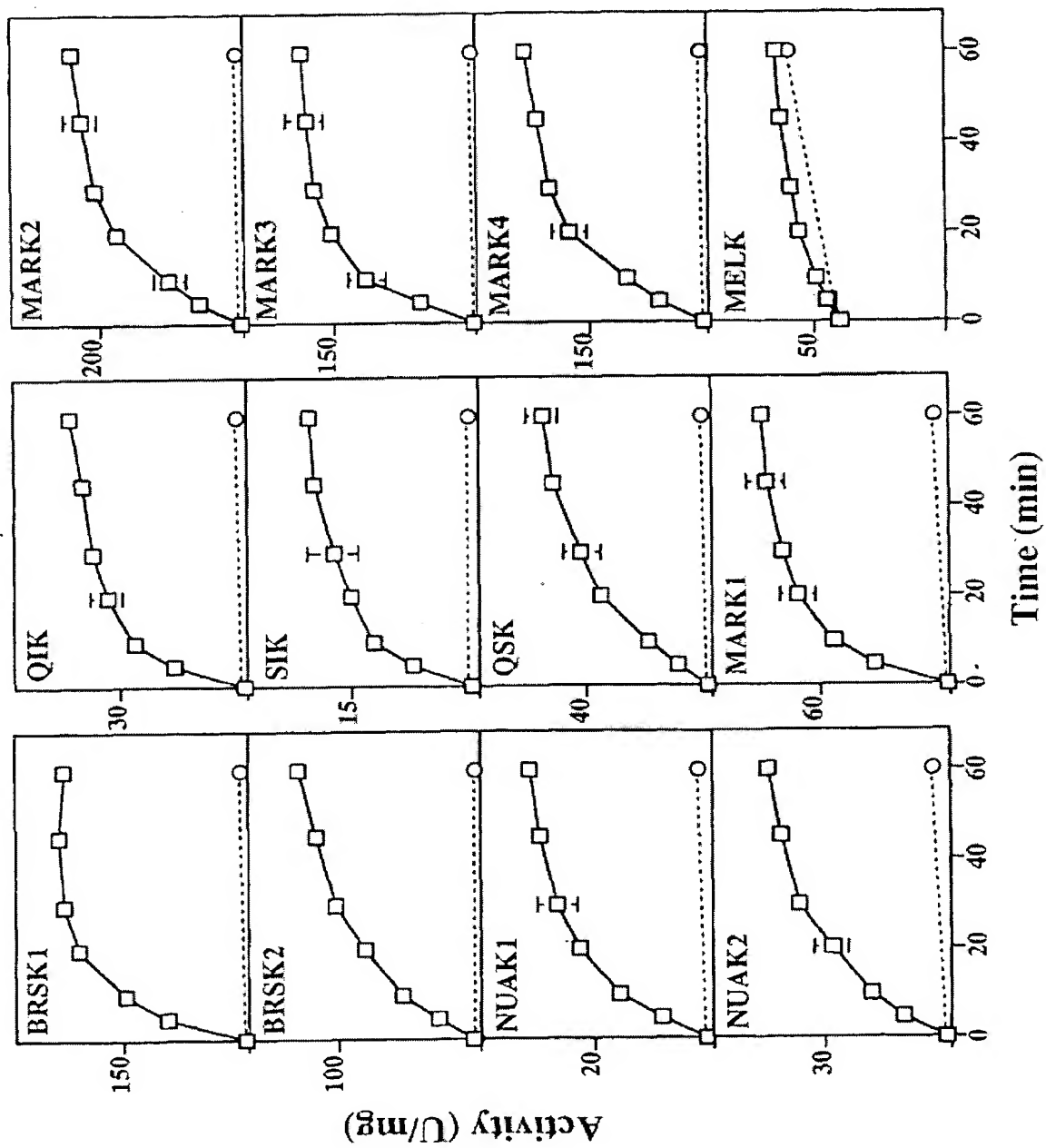


Figure 26A

Peptide				K _m (mM)	V _{max} (U/mg)	V _{max} /K _m
NUAK2	LSNLYHQGKFLQTFCGSPLYRRR	(SEQ ID NO:83)				
SIK	FGNFYKSGEPLSTWCGSPPYRRR	(SEQ ID NO:84)		0.15 ± 0.02	86.8 ± 3.4	578
AMPK	LSNMMSDGEFLRTSCGSPNYRRR	(SEQ ID NO:85)		0.46 ± 0.05	63.9 ± 2.2	139
BRSK2	MASLQVGDSLLETSCGSPHYRRR	(SEQ ID NO:86)		1.40 ± 0.24	94.1 ± 8.3	67
MARK3	MASLQVGDSLLETSCGSPHYRRR	(SEQ ID NO:87)		0.40 ± 0.06	10.6 ± 0.6	26
MELK	FSNEFTVGGKLDFTFCGSPPYRRR	(SEQ ID NO:88)		0.62 ± 0.06	10.2 ± 0.4	16
	AKPKGNDYHLQTCGSLAYRRR	(SEQ ID NO:88)		>3	>60	

Figure 26B

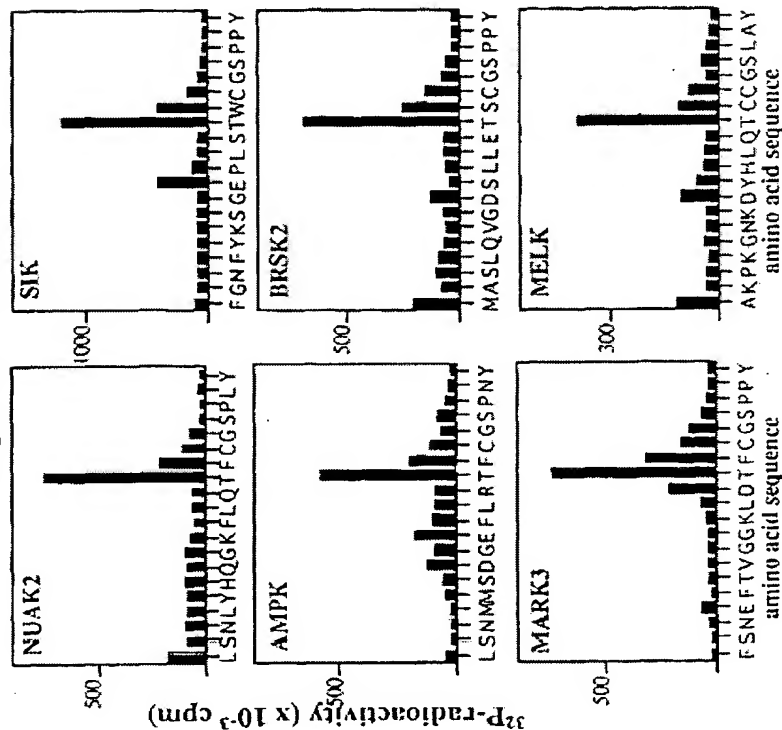


Figure 26C

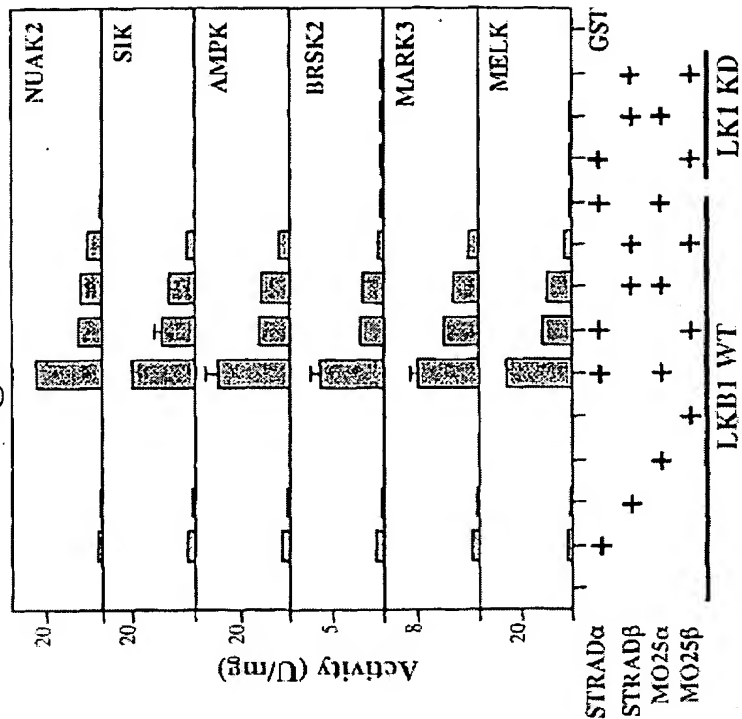


Figure 30A

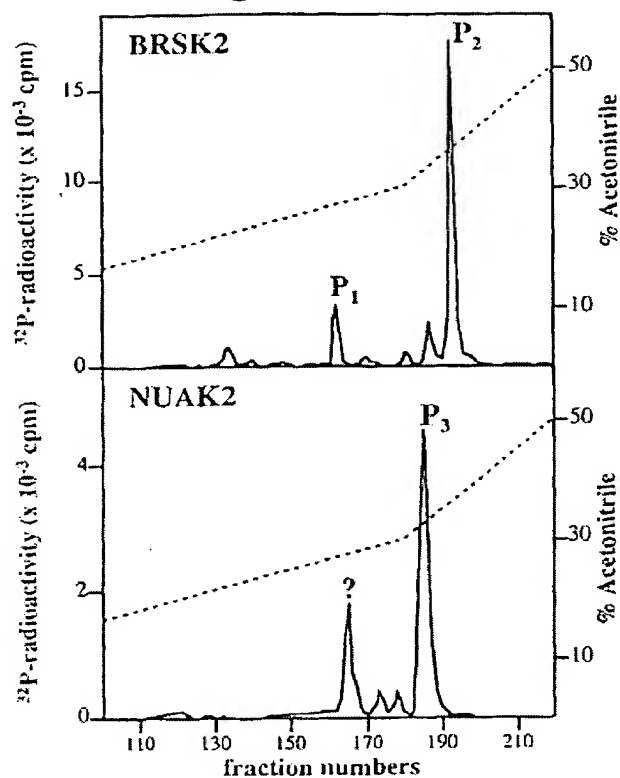


Figure 30B

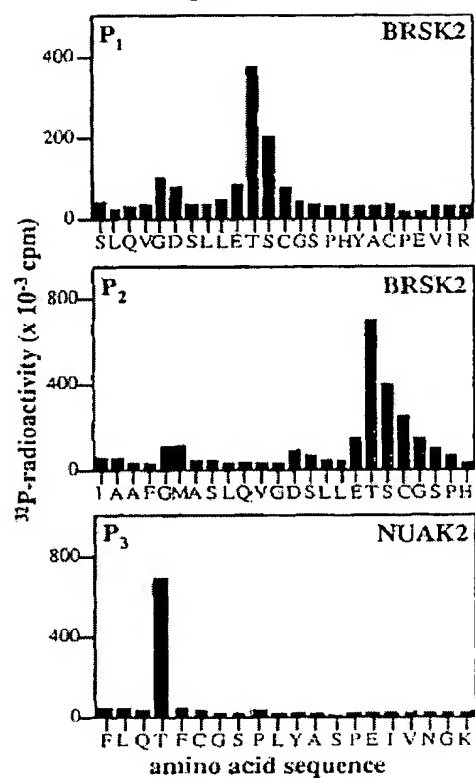


Figure 30C

Kinase	Posphopeptide	Mass observed	Theoretical mass
BRSK2 P_1	IAAFGmASLQVGDSLLET(p)SCGSPHYACPEVIR (SEQ ID NO:89)	3268.7870	3628.6680
BRSK2 P_2	SLQVGDSLLET(p)SCGSPHYACPEVIR (SEQ ID NO:90)	2951.4530	2951.3472
NUAK2 P_3	FLQT(p)FCGSPLYASPEIVNGK (SEQ ID NO:91)	2356.1088	2356.1333
MARK4	LDT(p)FCGSPPYAAPELFQ GK (SEQ ID NO:92)	2225.9983	2226.1497
MELK	GNKDYHLQT(p)CCGSLAYAAPELIQCK (SEQ ID NO:93)	2970.4421	2970.3648